

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

1. (Currently amended) A composition comprising an orthogonal glutamyl-tRNA (glutamyl O-tRNA) ~~derived from one or more archaeal tRNAs~~, wherein the glutamyl O-tRNA comprises ~~at the polynucleotide sequence of at least 80% identical to SEQ ID NO.: 67 or is transcribed from a complementary polynucleotide sequence thereof;~~

and ~~wherein the glutamyl O-tRNA suppresses in the presence of a glutamyl-~~ tRNA synthetase ~~derived from an (RS)~~ selected from the group consisting of: an *Archaeoglobus fulgidus* synthetase, a *Methanoscincus mazei* synthetase, a *Methanobacterium thermoautotrophicum* synthetase, and a *Pyrococcus horikoshii* synthetase.

2. (Cancelled)

3. (Currently amended) The composition of claim 1, ~~further comprising a wherein the selector codon that is an amber codon.~~

4. (Cancelled)

5. (Currently amended) The composition of claim 1, wherein the glutamyl-tRNA synthetase preferentially aminoacylates the glutamyl O-tRNA with a selected amino acid in response to ~~the-a~~ selector codon.

6. (Currently amended) The composition of claim 5, wherein ~~the-a~~ suppression efficiency of the glutamyl-tRNA synthetase and the glutamyl O-tRNA together is 4 to 5-fold greater than ~~a~~ ~~the~~ suppression efficiency of the glutamyl O-tRNA in the absence of the glutamyl-tRNA synthetase.

7. (Cancelled)

8. (Currently amended) The composition of claim 5, wherein the glutamyl-tRNA synthetase comprises an amino acid sequence comprising any one of SEQ ID NO.: 69 (AfRS), SEQ ID NO.: 73 (MmRS), SEQ ID NO.: 75 (MtRS), or SEQ ID NO.: 77 (PhRS).

9. (Cancelled)

10. (Cancelled)

11. (Cancelled)

12. (Original) The composition of claim 1, comprising a cell.

13. (Original) The composition of claim 12, wherein the cell is an *E. coli* cell.

14. (Original) The composition of claim 1, comprising a translation system.

15. (Currently amended) A cell comprising a translation system, wherein the translation system comprises:

an orthogonal glutamyl-tRNA (glutamyl O-tRNA), ~~derived from one or more archaeal tRNAs, wherein the glutamyl O-tRNA comprises at the polynucleotide sequence of at least 80% identical to~~ SEQ ID NO.: 67 ~~or is transcribed from a complementary polynucleotide sequence thereof;~~

a glutamyl-tRNA synthetase derived from an tRNA synthetase (RS) selected from the group consisting of: SEQ ID NO.: 69 (AfRS), SEQ ID NO.: 73 (MmRS), SEQ ID NO.: 75 (MtRS) and SEQ ID NO.: 77 (PhRS) ~~an Archaeoglobus fulgidus synthetase, a Methanosarcina mazei synthetase, a Methanobacterium thermoautotrophicum synthetase, and a Pyrococcus horikoshii synthetase; and,~~

a first selected amino acid;

wherein the glutamyl O-tRNA recognizes a first selector codon, and the glutamyl-tRNA synthetase preferentially aminoacylates the glutamyl O-tRNA with the first selected amino acid.

16. (Cancelled)

17. (Cancelled)

18. (Previously presented) The cell of claim 15, wherein the cell further comprises an additional different O-tRNA/tRNA synthetase pair and a second selected amino acid, wherein the additional O-tRNA recognizes a second selector codon and the additional tRNA synthetase preferentially aminoacylates the additional O-tRNA with the second selected amino acid.

19. (Cancelled)

20. (Original) The cell of claim 15, wherein the cell is a non-eukaryotic cell.

21. (Original) The cell of claim 20, wherein the non-eukaryotic cell is an *E. coli* cell.

22. (Currently amended) The cell of claim 15, further comprising a nucleic acid that comprises a polynucleotide that translates into ~~encodes~~ a polypeptide of interest, wherein the polynucleotide comprises a selector codon that is recognized by the glutamyl O-tRNA.

23. (Currently amended) An *E. coli* cell, comprising:

an orthogonal glutamyl tRNA (glutamyl O-tRNA), wherein the glutamyl O-tRNA comprises ~~at the polynucleotide sequence of at least 80% identical to SEQ ID NO.: 67 or is transcribed from a complementary polynucleotide sequence thereof;~~

a glutamyl-tRNA synthetase, wherein the glutamyl-tRNA synthetase preferentially aminoacylates the glutamyl O-tRNA with a selected amino acid;

the selected amino acid; and,

a nucleic acid that comprises a polynucleotide that encodes a polypeptide of interest, wherein the polynucleotide comprises the selector codon that is recognized by the glutamyl O-tRNA, and wherein ~~the glutamyl O-tRNA is derived from one or more archaeal tRNAs and the glutamyl-tRNA synthetase comprises is derived from an glutamyl-RS selected from the group consisting of: an *Archaeoglobus fulgidus* (Af) synthetase SEQ ID NO.: 69, a *Methanosarcina mazei* (Mm) synthetase SEQ ID NO.: 73, a *Methanobacterium thermoautotrophicum* (Mt) synthetase SEQ ID NO.: 75, and a *Pyrococcus horikoshii* (Ph) synthetase SEQ ID NO.: 77.~~